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TGURE

-MSWRGR-STYRPRPRRYVEPPEMIGPMRP-EQFSDEVEPATPEEGEPATQRQDPAAAQE -MSWRGR-STYRPRPRRYVEPPEMIGPMRP-EQFSDEVEPATPEEGEPATQRQDPAAAQE	MNLSRGKSTYYWPRPRRYVQPPEVIGPMRP-EQFSDEVEPATPEEGEPATQRQDPAAAQE -MSWRGRSTYYWPRPRRYVQPPEMIGPMRP-EQFSDEVEPATPEEGGEPATQRQDPAAAQE	-MSWRGRSTYYWPRPRRYVQPPEVIGPMRP-EQFSDEVEPATPEEGEPATQRQDPAAAQE	-mswrgrstyywprprryvQppenigpmrp-eQfsdevepatpeegepatQrOdpaaAQE -mswrgrstyywprprryvOppemigpmrp-EOfsdevepatpeegepatorodpaaAoe	-MSWRGRSTYYWPRPRRYVÕPPEMIGPMRP-EÕFSDEVEPATPEEGEPATÕRÕDPAAAÕE	-MSWRGR-STYRPRPRRYVEPPEMIGPMRP-EQFSDEVEPATPEEGGEPATQRQDPAAAQE	-MSWRGRSTIIWERFRRIOUPPENIGEMRF-EQFSDEVEFAIFEEGEFATURDFAAAQE -MSWRGR-STYRPRPRRSLOPPELIGAMLTGSPLSOEPTDEEPKEEKPPTKSRNPTPDOK	-MIWRGR-STYRPRPRRSVPPPELIGPMLEPGDEEPQQEEPPTESRDPAPGQE **:: :* **:: :*:: *;: *;	GE-DEGASAGQGPKPEADSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEE-EMRSHY	GE-DEGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGEKQSQC	GE-DEGASAGQGPKPEADSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGEKQSQC	GE-DEGASAGQGPKPEADSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGEKQSQC	GE-DEGASAGQGPKPEADSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGEKQSQC	GE-DEGASAGQGPKPEADSQEQGHPQTGCECEDGPDGQEVDPPNPEEVKTPEEGEKQSQC	GE-DEGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGEKQSQC	GE-DEGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGEKQSQC	GE-DEGASAGQGPKPEADSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGEKQSQC	GE-DEGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGEKQSQC	REDDQGAAEIQVPDLEADLQELCQTKTGDGCEGGTDVKGKILPKAEHFKMPEAGEGKSQV	REEDQGAAETQVPDLEADLQELSQSKTGGECGNGPDDQGKILPKSEQFKMPEGGDRQPQV	VAQTGILWLLMNNCFLNLSPRKP
GAGE-1 GAGE-2	GAGE-3 GAGE-4	GAGE-5	GAGE-6 GAGE-7	GAGE-7B	GAGE-8	1+2_ORF1 ;_ORF1	+2_ORF1	GAGE-1	GAGE-2	GAGE-3	GAGE-4	GAGE-5	GAGE-6	GAGE-7	GAGE-7B	GAGE-8	1+2_ORF1	2_ORF1	+2_ORF1	GAGE-1
g914899 g914901	g914903 g914905	g914907	g914909 g3300090	g3511025	g3511023	4030354CB1+2_ORF1 980547.1+2_ORF1	064516CB1+2_ORF1	g914899	g914901	g914903	g914905	g914907	g914909	g3300090	g3511025	g3511023	4030354CB1+2_ORF	980547.1+2_ORF1	064516CB1+2_ORF1	g914899

MPLEQRSQHCKPEEGLEARGEALGLVGAQAPATEEQEAASSSS-TLVEVTLGEVPAAESP MPLEQRSQHCKPEEGLEARGEALGLVGAQAPATEEQEAASSSS-TLVEVTLGEVPAAESP MPLEQRSQHCKPEEGLEARGEALGLVGAQAPATEEQEAASSSS-TLVEVTLGEVPAAESP MPLEQRSQHCKPEEGLEARGEALGLVGAQAPATEEQEAASSSS-TLVEVTLGEVPAAESP	MPLEQRSQHCKPEEGLEARGEALGLVGAQAPATEEQQTASSSS-TLVEVTLGEVPAADSP MPLEQRSQHCKPEEGLEARGEALGLVGAQAPATEEQQTASSSS-TLVEVTLGEVPAADSP MPLEQRSQHCKPEEGLEARGEALGLVGAQAPATEEQQTASSSS-TLVEVTLGEVPAADSP	MPLEQRSQHCKPEEGLEAQGEALGLVGAQAPATEEQETASSSS-TLVEVTLREVPAAESP MPLEQRSQHCKPEEGLEAQGEALGLVGAQAPATEEQETASSSS-TLVEVTLREVPAAESP MSSEOKSOHCKPEEGVEAOEEALGLVGAOAPTTEEOEAAVSSSSPLVPGTLERVPAAESA	MSSEQKSÖHCKPEEGVEAQEEALGLVGAQAPTTEEQEAAVSSSSPLVPGTLEEVPAAESA MSSEQKSQHCKPEEGVEAQEEALGLVGAQAPTTEEQEAAVSSSSPLVPGTLEEVPAAESA	HISSEÇASÇACKFEEGVEAÇEEALGLVGAÇAF 1 LEEQEAAVSSSSFLVFGILEEVFAAESA MSLEQKSQHCKPEEGVEAQEEALGLVGAQAPTTEEQEAAVSSSSPLVLGTLEKVPAAESA MPLEORSOHCKPEEGLOAOEEDLGLVGAOALOAEEOEAAFFSS-TLNVGTLEELPAAESP	MSLEQRSPHCKPDEDLEAĞGEDLGLMGAĞEPTGEEEETTSSDSKEEEVSAAGSS MPLEQRSQHCKPEEGLEARGEALGLVGAQAPATEEQEAASSSS-TLVEVTLGEVPAAESP MSLEQRSPHCKPDEDLEAQGEDLGLMGAQEPTGEEEETTSSSDSKEEEVSAAGSS * * * * * * * * * * * * * * * * * * *		DPPQSPQGASSLPTTMNYPLWSQSYEDSSNQEEEGPSTFPDLESEFQAALSRKVAEL DPPQSPQGASSLPTTMNYPLWSQSYEDSSNQEEEGPSTFPDLESEFQAALSRKVAEL	SPPHSPQGASSFSTTINYTLWRQSDEGSSNQEEEGPRMFPDLESEFQAAISRKMVEL SPPHSPOGASSFSTTINYTLWROSDEGSSNOEEEGPRMFPDLESEFOAAISRKMVEL	1 1		GPPQSPQGASALPTISFTCWRQPNEGSSSQEEEGPSTSPDAESLFREALSNKVDEL	GPPQSPQGASALPTTISFTCWRQPNEGSSSQEEEGPSTSPDAESLFREALSNKVDEL GPPOGPOGAGALDTTISFTCWRODNFGGGGOFFFGDGTGDDAFGLFREALSNKVDET	GPPQSPQGASALPTTISFTCWRQPNEGSSSQEEEGPSTSPDAESLFREALSNKVDEL	DPPQSPQGASALPTISFTCWRQPNEGSSSQEEEEASTSPDAESLFREALSNKVDEL	SPPQSPQEESFSPTAMDAIFGSLSDEGSGSQEKEGPSTSPDLIDPESFSQDILHDKIIDL	SPPQSPQGGASSSISVYYTLWSQFDEGSSSQEEEEPSSSVDPAQLEFMFQEALKLKVAEL	DPPQSPQGASSLPTTMNYPLWSQSYEDSSNQEEEGPSTFPDLESEFQAALSRKVAKL SPPQSPQGGASSSISVYYTLWSQFDEGSSSQEEEEPSSSVDPAQLEFMFQEALKLKVAEL
MAGE-3B MAGE-6 MAGE-A3 MAGE-3	MAGE-A2b MAGE-A2a MAGE-2	MAGE-A12 MAGE-12 MAGE-4b	MAGE-X2 MAGE-41	MAGE-49 MAGE-4 MAGE-11	MAGE-9 1_ORF1 ORF1	MAGE-3B MAGE-6	MAGE-A3 MAGE-3	MAGE-A2b MAGE-A2a	MAGE-2	MAGE-12	MAGE-4b	MAGE-X2 MAGE-41	MAGE-4a	MAGE-4		MAGE-9	.1_ORF1 ORF1
9499122 9533523 97280335 9468826	g7280334 g7280332 g436181	g7280333 g499346 q533517	9499124 91125018	g333513 g1125014 g533513	g533528 MAGE 1471808CB1+1_ORF 1097797.1+1_ORF1	g499122 g533523	g7280335 g468826	g7280334 q7280332	g436181	9499346	g533517	g499124 g1125018	g533515	g1125014	g533513	g533528	1471808CB1+1_ORF 1097797.1+1_ORF1

Inventors: Jones et al. Title: GENES REGULATED BY DNA METHYLATION IN TUMOR CELLS Serial No.: To Be Assigned

LQLVFGIELMEVDPIGHVY LQLVFGIELMEVDPIGHVY LQLVFGIELMEVDPIGHLY LQLVFGIELMEVDPIGHLY LQLVFGIELWEVDPIGHLY LQLVFGIEVVEVVPISHLY LQLVFGIEVVEVVPISHLY LQLVFGIEVVEVVPISHLY LQLVFGIEVVEVVPISHLY LQLVFGIEVVEVVPISHLY LQLVFGIEVVEVVPISHLY LKMIFGIDVKEVDPTSNTY LKMIFGIDVKEVDPTSNTY LKMIFGIDVKEVDPTSNTY LKMIFGIDVKEVDPASNTY LKMIFGIDVKEVDPASNTY LKMIFGIDVKEVDPASNTY LKMIFGIDVKEVDPASNTY LKMIFGIDVKEVDPASNTY LKMIFGIDVKEVDPASNTY MQLLFGIDVKEVDPASNTY MQLLFGIDVKEVDPAGHSY LQLVFGIELMEVDPIGHLY MQVIFGTDVKEVDPAGHSY LQLVFGIELMEVDPIGHSY LXMIFGIDVKEVDPAGHSY LXMIFGIDVKEVDPAGHSY LQLVFGIELMEVDPIGHLY	VEELSVLEVFEGRED VEELSVLEVFEGRED VEELSVLEVFEGRED VEELSMLEVFEGRED VEELSMLEVFEGRED VEELSMLEVFEGRED VEELSMLEVFEGRED VEELSMLEVFEGRED VEELSVLEASDGRED VEELGVMGVYDGREH
NWQYFFPVIFSKASDSLQLV NWQYFFPVIFSKASSSLQLV NWQYFFPVIFSKASSSLQLV NWQYFFPVIFSKASSSLQLV NCQDFFPVIFSKASEYLQLV NCQDFFPVIFSKASEYLQLV NCQDFFPVIFSKASEYLQLV NCQDFFPVIFSKASEYLQLV NYQDFFPVIFSKASEYLQLV NYKRCFPVIFGKASESLKMI NYKRYFPVIFGKASESLKMI NYKRYFPVIFGKASESLKMI NYKRYFPVIFGKASEFMQVI NYKRYFPVIFGKASEFM	LIIILAIIAKEGDCAPEEKI LIIILAIIAKEGDCAPEEKI LIIVLAIIAREGDCAPEEKI LIIVLAIIAREGDCAPEEKI LIIVLAIIAIEGDCAPEEKI LIIVLAIIAIEGDCAPEEKI LIIVLAIIAKEGDCAPEEKI LIIVLAIIAKEGDCAPEEKI LIIVLGTIAMEGDSASEEEI LIIVLGTIAMEGDSASEEEI LIIVLGTIAMEGDSASEEEI LIIVLGTIAMEGDSASEEEI LIIVLGTIAMEGDSASEEEI LIIVLGVIFMEGNCIPEEVM LIIVLGVIFMEGNCIPEEVM
VHFLLLKYRAREPVTKAEMLGSVVGNWQYFFPVIFSKASDSLQLVFGIELMEVDPIGHVY VHFLLLKYRAREPVTKAEMLGSVVGNWQYFFPVIFSKASDSLQLVFGIELMEVDPIGHLY VHFLLLKYRAREPVTKAEMLGSVVGNWQYFFPVIFSKASSSLQLVFGIELMEVDPIGHLY VHFLLLKYRAREPVTKAEMLGSVVGNWQYFFPVIFSKASSSLQLVFGIELMEVDPIGHLY VHFLLLKYRAREPVTKAEMLGSVVGNWQYFFPVIFSKASSSLQLVFGIELWEVDPIGHLY VHFLLLKYRAREPVTKAEMLGSVVGNWQYFFPVIFSKASEYLQLVFGIELVEVVEVVPISHLY VHFLLLKYRAREPVTKAEMLESVLRNCQDFFPVIFSKASEYLQLVFGIEVVEVVPISHLY VHFLLLKYRAREPVTKAEMLGSVIRNFQDFFPVIFSKASEYLQLVFGIEVVEVVVRIGHLY VHFLLLKYRAREPYTKAEMLGSVIRNFQDFFPVIFSKASEYLQLVFGIEVVEVVVRIGHLY VHFLLLKYRAREPYTKAEMLGSVIRNYKRCFPVIFGKASESLKMIFGIDVKEVDPTSNTY AHFLLRKYRAKELVTKAEMLERVIKNYKRCFPVIFGKASESLKMIFGIDVKEVDPTSNTY AHFLLRKYRAKELVTKAEMLERVIKNYKRCFPVIFGKASESLKMIFGIDVKEVDPASNTY AHFLLRKYRAKELVTKAEMLESVIKNYKRCFPVIFGKASESLKMIFGIDVKEVDPASNTY VHFLLLKKYRAKELVTKAEMLESVIKNYKRYFPVIFGKASESLKMIFGIDVKEVDPAGHSY VHFLLLKKYRAKEPVTKAEMLESVIKNYKRYFPVIFGKASESLKMIFGIDVKEVDPAGHSY VHFLLLKYRAREPVTKAEMLESVIKNYKRYFPVIFGKASEFMQVIFGTDVKEVDPAGHSY VHFLLLKYRAREPVTKAEMLESVIKNYKRYFPVIFGKASEFMQVIFGTDVKEVDPAGHSY VHFLLLKYRARVENVKEPVTKAEMLESVIKNYKRYFPVIFGKASEFMQVIFGTDVKEVDPAGHSY VHFLLLKYRARVENVKEPVTKAEMLESVIKNYKRYFPVIFGKASEFMQVIFGTDVKEVDPAGHSY ************************************	IFATCLGLSYDGLLGDNQIMPKTGFLIIILAIIAKEGDCAPEEKIWEELSVLEVFEGRED IFATCLGLSYDGLLGDNQIMPKTGFLIIILAIIAKEGDCAPEEKIWEELSVLEVFEGRED IFATCLGLSYDGLLGDNQIMPKAGLLIIVLAIIAKEGDCAPEEKIWEELSVLEVFEGRED IFATCLGLSYDGLLGDNQIMPKAGLLIIVLAIIAREGDCAPEEKIWEELSVLEVFEGRED ILVTCLGLSYDGLLGDNQIMPKTGLLIIVLAIIAIEGDCAPEEKIWEELSWLEVFEGRED ILVTCLGLSYDGLLGDNQWPKTGLLIIVLAIIAIEGDCAPEEKIWEELSWLEVFEGRED ILVTCLGLSYDGLLGDNQUMPKTGLLIIVLAIIAKEGDCAPEEKIWEELSWLEVFEGRED ILVTCLGLSYDGLLGDNQINPKTGLLIIVLAIIAKEGDCAPEEKIWEELSVLEASDGRED ILVTCLGLSYDGLLGNNQIPFYTGLLIIVLAIIAMEGDSASEEEIWEELGVMGVYDGREH TLVTCLGLSYDGLLGNNQIFPKTGLLIIVLGTIAMEGDSASEEEIWEELGVMGVYDGREH TLVTCLGLSYDGLLGNNQIFPKTGLLIIVLGTIAMEGDSASEEEIWEELGVMGVYDGREH TLVTCLGLSYDGLLGNNQIFPKTGLLIIVLGTIAMEGDSASEEEIWEELGVMGVYDGREH TLVTCLGLSYDGLLGNNQIFPKTGLLIIVLGTIAMEGDSASEEEIWEELGVMGVYDGREH TLVTCLGLSYDGLLGNNQIFPKTGLLIIVLGTIAMEGDSASEEEIWEELGVMGVYDGREH TLVTCLGLSYDGLLGNNQIFPKTGLLIIVLGTIAMEGDSASEEEIWEELGVMGVYDGREH TLVTCLGLSYDGLLGNNQIFPKTGLLIIVLGTIAMEGDSASEEIWEELGVMGVYDGREH TLVTTCLGLSYDGLLGNNQIFPKTGLLIIVLGTIAMEGDSASEEEIWEELGVMGVYDGREH TLVTTCLGLSYDGLLGNNQIFPKTGLLIIVLGTIAMEGDSASEEEIWEELGVMGVYDGREH TLVTTCLGLSYDGLLGNNQIFPKTGLLIIVLGTIAMEGDSASEEEIWEELGVMGVYDGREH TLVTTCLGLSYDGLLGNNQIFPKTGLLIIVLGTIAMEGDSASEEEIWEELGVMGVYDGREH TLVTTCLGLSYDGLLGNNQIFPKTGLLIIVLGTIAMEGDSASEEEIWEELGVMGVYDGREH TLVTTCLGLSYDGLLGNNQIFPKTGLLIIVLGTIAMEGDSASEEEIWEELGVMGVYDGREH TLVTTCLGLSYDGLLGNNQIFPKTGLLIIVLGTIAMEGDSASEEEIWEELGVMGVYDGREH TLVTTCLGLSYDGLLGNNQIFPKTGLLIIVLGTIAMEGDSASEEEIWEELGVMGVYDGREH TLVTTCLGLSYDGLLGNNQITFFTGLLIIVLGTIAMEGDSASEEIWEELGVMGVYDGREH TLVTTCLGLSYDGLLGNNQITFTGLLIIVLGTIAMEGDSASEEIWEELGVMGVYDGREH TLVTTCLGLSYDGLLGNNQITFTGLLIIVLGTIAMEGDSASEEIWEELGVMGVYDGREH TLVTTCLGLSYDGLLGNNQITTGLTIIVLGTIAMEGDSASEEIWEELGVMGVYDGREH TLVTTCLGLSYDGLGNNQITTGLTIILTAIIAKEGDC
3B 6 6 3 3 3 A2b 2 2 2 2 11 12 44 44 44 44 9	3B 6 6 73 3 3 42b 72b 72 72 712 44 44 44 41 111
9499122 MAGE- 9533523 MAGE- 9468826 MAGE- 97280334 MAGE- 97280332 MAGE- 97280332 MAGE- 97280333 MAGE- 97280333 MAGE- 97280333 MAGE- 9533517 MAGE- 9533515 MAGE- 9533515 MAGE- 9533515 MAGE- 9533515 MAGE- 9533513 MAGE- 9533513 MAGE- 9533513 MAGE- 9533513 MAGE- 97797.1+1_ORF1	9499122 MAGE- 9533523 MAGE- 97280335 MAGE- 97280334 MAGE- 97280332 MAGE- 97280332 MAGE- 97280333 MAGE- 97280333 MAGE- 9533517 MAGE- 9533515 MAGE- 9533515 MAGE- 9533515 MAGE- 9533513 MAGE- 9533513 MAGE- 9533513 MAGE- 9533513 MAGE- 9533513 MAGE-

FIGURE 2C

1097797.1+1_ORF1	1471808CB1+1_ORF1	g533528 MAGE-9	g533513 MAGE-11	g1125014 MAGE-4	g533515 MAGE-4a	g1125018 MAGE-41	g499124 MAGE-X2	g533517 MAGE-4b	g499346 MAGE-12	g7280333 MAGE-A12	g436181 MAGE-2	g7280332 MAGE-A2a	g7280334 MAGE-A2b	g468826 MAGE-3	. 1	g533523 MAGE-6	g499122 MAGE-3B
EPICYPSLYEEVLGEEQEGV	PRISYPLLHEWALREGEE	EPICYPSLYEEVLGEEQEGV	1 DPTSYPSLYEDALREEGEGV	VRIAYPSLREAALLEEEEGV	la VRIAYPSLREAALLEEEEGV	11 VRIAYPSLREAALLEEEEGV	VRIAYPSLRQAALLEEEGV	lb VRIAYPSLREAALLEEEEGV	.2 PHIPYPPLHEWAFREGEE	12 PHISYPPLHEWAFREGEE	PHISYPPLHERALREGEE	12a PHISYPPLHERALREGEE	12b PHISYPPLHERALREGEE	PHISYPPLHEWVLREGEE	13 PHISYPPLHEWVLREGEE	PRISYPLLHEWALREGEE	B PRISYPLLHEWALREGEE

097797.1+1	471808CB1+	53352	53351	11250	g533515	11250	49912	53351	49934	72803	43618	728033	72803	46882	72803	53352	49912
_ORF1	1_ORF1	MAGE-9	MAGE-11	MAGE-4	MAGE-4a	1	MAGE-X2	- 1	MAGE-12	MAGE-A12	1	MAGE-A2a	MAGE-A2b	MAGE-3	MAGE-A3	MAGE-6	MAGE-3B
MFY	SII	MFY	FLF	ŢVŢ	ŢV	Ϋ́	Ϋ́	ZVI.	SVF	SVF	SVF	SVF	SVE	SII	SII	SII	SIF

MFYGEPRKLLTQDWVQENYLEYRQVPGSDPAHYEFLWGSKAHAETSYEKVINYLVMLNAR SILGDPKKLLTQHFVQENYLEYRQVPGSDPACYEFLWGPRALVETSYVKVLHHMVKISGG MFYGEPRKLLTQDWVQENYLEYRQVPGSDPAHYEFLWGSKAHAETSYEKVINYLVMLNAR *::** * ***:** ******::* **** ***	TVYGEPRKLLTQDWVQENYLEYRQVPGSNPARYEFLWGPRALAETSYVKVLEHVVRVNAR TVYGEPRKLLTQDWVQENYLEYRQVPGSNPARYEFLWGPRALAETSYVKVLEHVVRVNAR TVYGEPRKLLTQDWVQENYLEYRQVPGSNPARYEFLWGPRALAETSYVKVLEHVVRVNAR FLFGEPKRLLTQNWVQEKYLVYRQVPGTDPACYEFLWGPRAHAETSKMKVLEYIANANGR	SVFAHPRKLLTQDLVQENYLEYRQVPGSDPACYEFLWGPRALVETSYVKVLHHLLKISGG SVFAHPRKLLTQDLVQENYLEYRQVPGSDPACYEFLWGPRALVETSYVKVLHHLLKISGG TVYGEPRKLLTQDWVQENYLEYRQVPGSNPARYEFLWGPRALAETSYVKVLEHVVRVNAR TVYGEPRKLLTQDWVQENYLEYRQVPGSNPARYEFLWGPRALAETSYVKVLEHVVRVNAR	SILGDPKKLLTQHFVQENYLEYRQVPGSDPACYEFLWGPRALVETSYVKVLHHMVKISGG SVFAHPRKLLMQDLVQENYLEYRQVPGSDPACYEFLWGPRALIETSYVKVLHHTLKIGGE SVFAHPRKLLMQDLVQENYLEYRQVPGSDPACYEFLWGPRALIETSYVKVLHHTLKIGGE SVFAHPRKLLMQDLVQENYLEYRQVPGSDPACYEFLWGPRALIETSYVKVLHHTLKIGGE	SIFGDPKKLLTQYFVQENYLEYRQVPGSDPACYEFLWGPRALIETSYVKVLHHMVKISGG SIFGDPKKLLTQYFVQENYLEYRQVPGSDPACYEFLWGPRALIETSYVKVLHHMVKISGG SILGDPKKLLTQHFVQENYLEYRQVPGSDPACYEFLWGPRALVETSYVKVLHHMVKISGG
INYLVMLNAR LHHMVKISGG INYLVMLNAR	LEHVVRVNAR LEHVVRVNAR LEHVVRVNAR LEYIANANGR	LHHLLKISGG LHHLLKISGG LEHVVRVNAR LEHVVRVNAR	LHHMVKISGE LHHTLKIGGE LHHTLKIGGE	LHHMVKISGG LHHMVKISGG

TIGETI SETTSOUT